

0590

OIPE

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/895,840

CRF Processing Date: 12/26/2001
Edited by: AN
Verified by: AN (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 2/1/95

RAW SEQUENCE LISTING

DATE: 12/26/2001

PATENT APPLICATION: US/09/895,840

TIME: 17:41:40

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\12262001\I895840.raw

4 <110> APPLICANT: Guenther, Catherine
 6 <120> TITLE OF INVENTION: Transgenic mice containing RORgamma gene
 7 disruptions
 9 <130> FILE REFERENCE: R-409
 11 <140> CURRENT APPLICATION NUMBER: US 09/895,840
 12 <141> CURRENT FILING DATE: 2001-06-28
 14 <150> PRIOR APPLICATION NUMBER: US 60/215,466
 15 <151> PRIOR FILING DATE: 2000-06-29
 17 <150> PRIOR APPLICATION NUMBER: US 60/221,667
 18 <151> PRIOR FILING DATE: 2000-07-27
 20 <160> NUMBER OF SEQ ID NOS: 4
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2066
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Mus musculus
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <222> LOCATION: 1527
 32 <223> OTHER INFORMATION: n = A,T,C or G
 34 <400> SEQUENCE: 1
 35 ggagggcagc aaggacggca ccaagggagc taccocatgg acagggcccc acagagacac 60
 36 caccggacat ctcgggagct gctggctgca aagaagacc acacctcaca aattgaagtg 120
 37 atcccttgca agatctgtgg ggacaagtca tctgggatcc actacggggt tatcacctgt 180
 38 gaggggtgca agggcttctt ccgcgcagc cagcagtgtg atgtggccta ctctgcaag 240
 39 cgtcagcaga actgccccat tgaccgaacc agccgaacc gatgccagca ttgcgcctg 300
 40 cagaagtgcc tggctctggg catgtcccgga gatgtgtgca agtttggccg aatgtccaag 360
 41 aagcagaggg acagtctaca tgcagaagtg cagaaacaac tgcaacagca gcagcaacag 420
 42 gaacaagtgg ccaagactcc tccagctggg agccgcggag cagacacact tacatacact 480
 43 ttagggctct cagatgggca gctaccactg ggcgcctcac ctgacctacc cgaggcctct 540
 44 gcttgctccc ctggcctcct gagagcctca ggctctggcc caccatattc caataccttg 600
 45 gccaaaacag aggtccaggg ggcctcctgc cacccttgagt atagtccaga acgaggcaaa 660
 46 gctgaaggca gagacagcat ctatagcact gacggccaac ttactcttgg aagatgtgga 720
 47 cttcgttttg aggaaaccag gcctcctgaa cttgggggaa cagaacaggg tccagacagc 780
 48 cactgcattc ccagtttctg cagtgcctca gaggtacct atgcctctct gacagacata 840
 49 gagtacctgg tacagaatgt ctgcaagtcc ttccgagaga catgccagct gcgactggag 900
 50 gaccttctac ggcagcgcac caacctcttt tcacgggagg aggtgaccag ctaccagagg 960
 51 aagtcaatgt gggagatgtg ggagcgtgtg gccaccacc tcactgaggc cattcagtat 1020
 52 gtggtggagt ttgccaagcg gctttcaggg ttcatggagc tctgccagaa tgaccagatc 1080
 53 atactactga cagcaggagc aatggaagtc gtccatagtc gaatgtgcag ggcctacaat 1140
 54 gccacaacc acacagtctt ttttgaaggc aaatacggtg gtgtggagct gtttcgagcc 1200
 55 ttgggctgca gcgagctcat cagctccata tttgactttt cccacttcct cagcgccttg 1260
 56 tgtttttctg aggatgagat tgccctctac acggccctgg ttctcatcaa tgccaaccgt 1320
 57 cctgggctcc aagagaagag gagagtggaa catctgcaat acaatttgga actggctttc 1380
 58 catcatcatc tctgcaagac tcatcgaaa ggcctcctag ccaagctgcc acccaaagga 1440
 59 aaactccgga gcctgtgcag ccaacatgtg gaaaagctgc agatcttcca gcacctccac 1500
 60 cccatcgtgg tccaagccgc cttcccncca ctctataagg aactcttcag cactgatgtt 1560

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61 gaatccccctg aggggctgtc aaagtgatct ggaggaagga caactttcta tttccttcag 1620
62 ccctctgacc cgtctccctg gactcccttc acccagcctt tccctttctg cactctatga 1680
63 aggggtggtat ccctaggagt aagcaaatcc taagactgat tttctgcccc taggcttgcc 1740
64 ttgtaggaca acagcagcaa gtgatggaga aaaggcttgt tatgtttgat ttcccataag 1800
65 ttccaccctg gcttctggaa gctgtggggt agatgggata gagataggat gaccaagtca 1860
66 aataaaaaaac agactgacaa tcagcagggg taaatccagg tacctgggat aaggagaact 1920
67 caaatctagg cttgaaagct aataacagtc ctttcaatac ctcattgtat ttcccatg 1980
68 gtctctctgg ggggacatgg atctagctca gagactggtg gcaagcccc agaaggacct 2040
69 gtatataata agaatataga ttctgt                                     2066
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72 <211> LENGTH: 516
73 <212> TYPE: PRT
74 <213> ORGANISM: Mus musculus
76 <400> SEQUENCE: 2
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78 1 5 10 15
79 Ala Ala Lys Lys Thr His Thr Ser Gln Ile Glu Val Ile Pro Cys Lys
80 20 25 30
81 Ile Cys Gly Asp Lys Ser Ser Gly Ile His Tyr Gly Val Ile Thr Cys
82 35 40 45
83 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Gln Gln Cys Asn Val Ala
84 50 55 60
85 Tyr Ser Cys Thr Arg Gln Gln Asn Cys Pro Ile Asp Arg Thr Ser Arg
86 65 70 75 80
87 Asn Arg Cys Gln His Cys Arg Leu Gln Lys Cys Leu Ala Leu Gly Met
88 85 90 95
89 Ser Arg Asp Ala Val Lys Phe Gly Arg Met Ser Lys Lys Gln Arg Asp
90 100 105 110
91 Ser Leu His Ala Glu Val Gln Lys Gln Leu Gln Gln Gln Gln Gln
92 115 120 125
93 Glu Gln Val Ala Lys Thr Pro Pro Ala Gly Ser Arg Gly Ala Asp Thr
94 130 135 140
95 Leu Thr Tyr Thr Leu Gly Leu Ser Asp Gly Gln Leu Pro Leu Gly Ala
96 145 150 155 160
97 Ser Pro Asp Leu Pro Glu Ala Ser Ala Cys Pro Pro Gly Leu Leu Arg
98 165 170 175
99 Ala Ser Gly Ser Gly Pro Pro Tyr Ser Asn Thr Leu Ala Lys Thr Glu
100 180 185 190
101 Val Gln Gly Ala Ser Cys His Leu Glu Tyr Ser Pro Glu Arg Gly Lys
102 195 200 205
103 Ala Glu Gly Arg Asp Ser Ile Tyr Ser Thr Asp Gly Gln Leu Thr Leu
104 210 215 220
105 Gly Arg Cys Gly Leu Arg Phe Glu Glu Thr Arg His Pro Glu Leu Gly
106 225 230 235 240
107 Glu Pro Glu Gln Gly Pro Asp Ser His Cys Ile Pro Ser Phe Cys Ser
108 245 250 255
109 Ala Pro Glu Val Pro Tyr Ala Ser Leu Thr Asp Ile Glu Tyr Leu Val
110 260 265 270
111 Gln Asn Val Cys Lys Ser Phe Arg Glu Thr Cys Gln Leu Arg Leu Glu

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112          275          280          285
113 Asp Leu Leu Arg Gln Arg Thr Asn Leu Phe Ser Arg Glu Glu Val Thr
114          290          295          300
115 Ser Tyr Gln Arg Lys Ser Met Trp Glu Met Trp Glu Arg Cys Ala His
116 305          310          315          320
117 His Leu Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Leu
118          325          330          335
119 Ser Gly Phe Met Glu Leu Cys Gln Asn Asp Gln Ile Ile Leu Leu Thr
120          340          345          350
121 Ala Gly Ala Met Glu Val Val Leu Val Arg Met Cys Arg Ala Tyr Asn
122          355          360          365
123 Ala Asn Asn His Thr Val Phe Phe Glu Gly Lys Tyr Gly Gly Val Glu
124          370          375          380
125 Leu Phe Arg Ala Leu Gly Cys Ser Glu Leu Ile Ser Ser Ile Phe Asp
126 385          390          395          400
127 Phe Ser His Phe Leu Ser Ala Leu Cys Phe Ser Glu Asp Glu Ile Ala
128          405          410          415
129 Leu Tyr Thr Ala Leu Val Leu Ile Asn Ala Asn Arg Pro Gly Leu Gln
130          420          425          430
131 Glu Lys Arg Arg Val Glu His Leu Gln Tyr Asn Leu Glu Leu Ala Phe
132          435          440          445
133 His His His Leu Cys Lys Thr His Arg Gln Gly Leu Leu Ala Lys Leu
134          450          455          460
135 Pro Pro Lys Gly Lys Leu Arg Ser Leu Cys Ser Gln His Val Glu Lys
136 465          470          475          480
137 Leu Gln Ile Phe Gln His Leu His Pro Ile Val Val Gln Ala Ala Phe
138          485          490          495
139 Pro Pro Leu Tyr Lys Glu Leu Phe Ser Thr Asp Val Glu Ser Pro Glu
140          500          505          510
141 Gly Leu Ser Lys
142          515
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 200
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Targeting vector
153 <400> SEQUENCE: 3
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155 gagaccagtg cacatgaatt ggaggtccct gggaccacct caaactccga gaggggtggga 120
156 taagcagttt ctgtttccca gggcttcttc cgccgcagcc agcagtgtaa tgtggcctac 180
157 tctgcacgc gtcagcagaa 200
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 200
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Targeting vector
167 <400> SEQUENCE: 4

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168 catacacttt agggctctca gatgggcagc taccactggg cgcctcacct gacctaccg 60
169 aggcctctgc ttgtccccct ggctcctga gagcctcagg ctctggccca ccattattcca 120
170 ataccttggc caaaacagag gtccaggggg cctcctgcca ccttgagtat agtccagaac 180
171 gaggcaaagc tgaaggcaga                                     200
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VERIFICATION SUMMARY

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L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1